# Loom Workflow Engine: Collaboration through portable, shareable data analysis

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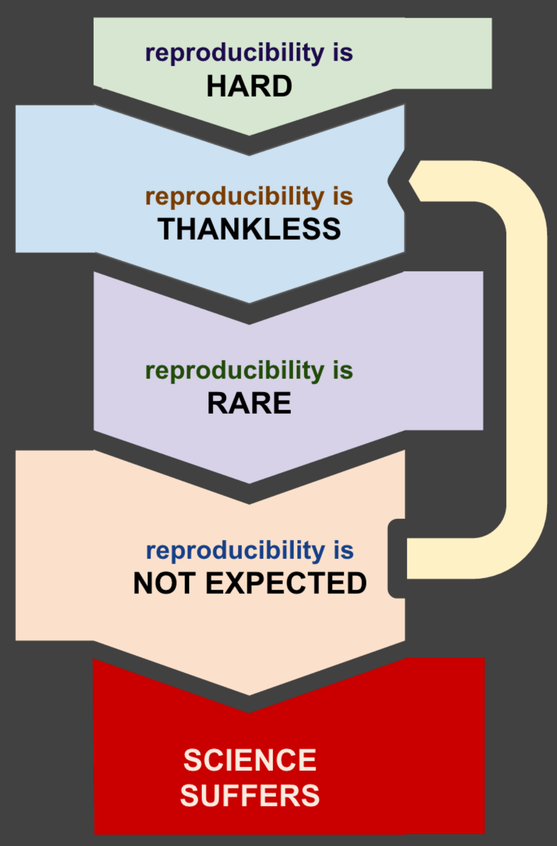
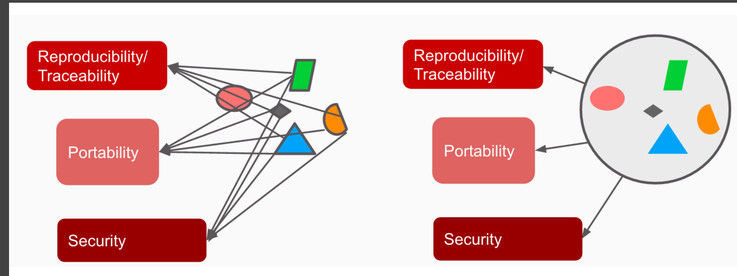
## ACADEMIC RESEARCH must be REPRODUCIBLE

**Think back to a computational result from 3 years ago**

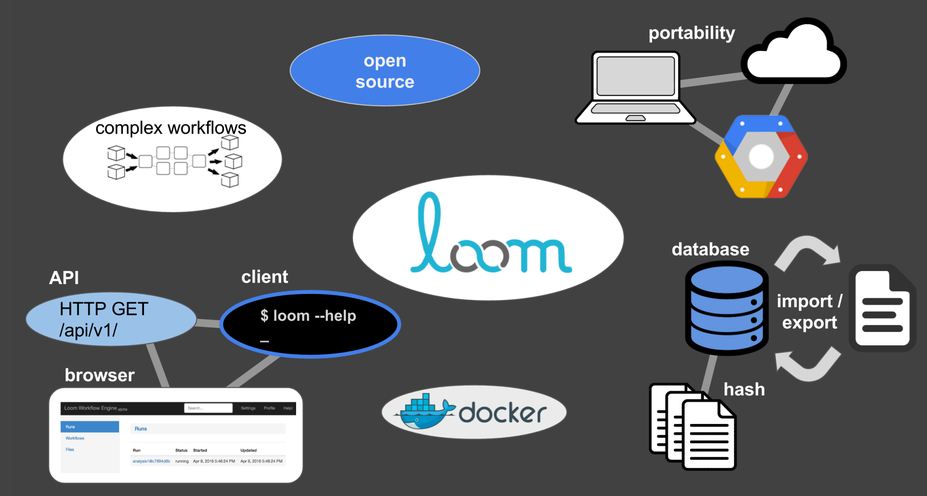
- **How did you generate this result?**
- **What was the input data? Can you verify it?**
- **What were the software versions? Are you sure?**
- **Can you rerun the analysis and verify the result?**
- **Can someone else run the analysis without your help?**




## Why use a workflow framework?

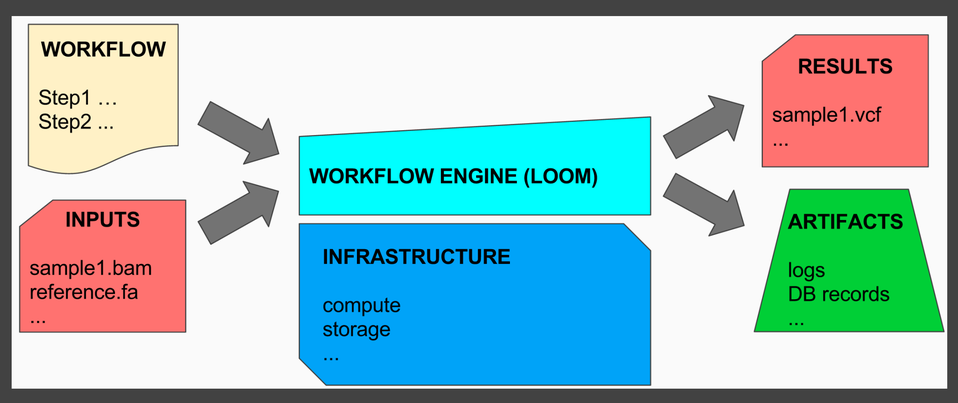



- A workflow framework can ensure reproducibility and implement other common functions in a consistent way across all steps.
- This is easier, cleaner, and safer than depending on the pipeline developer to implement these functions for every step in in every workflow.

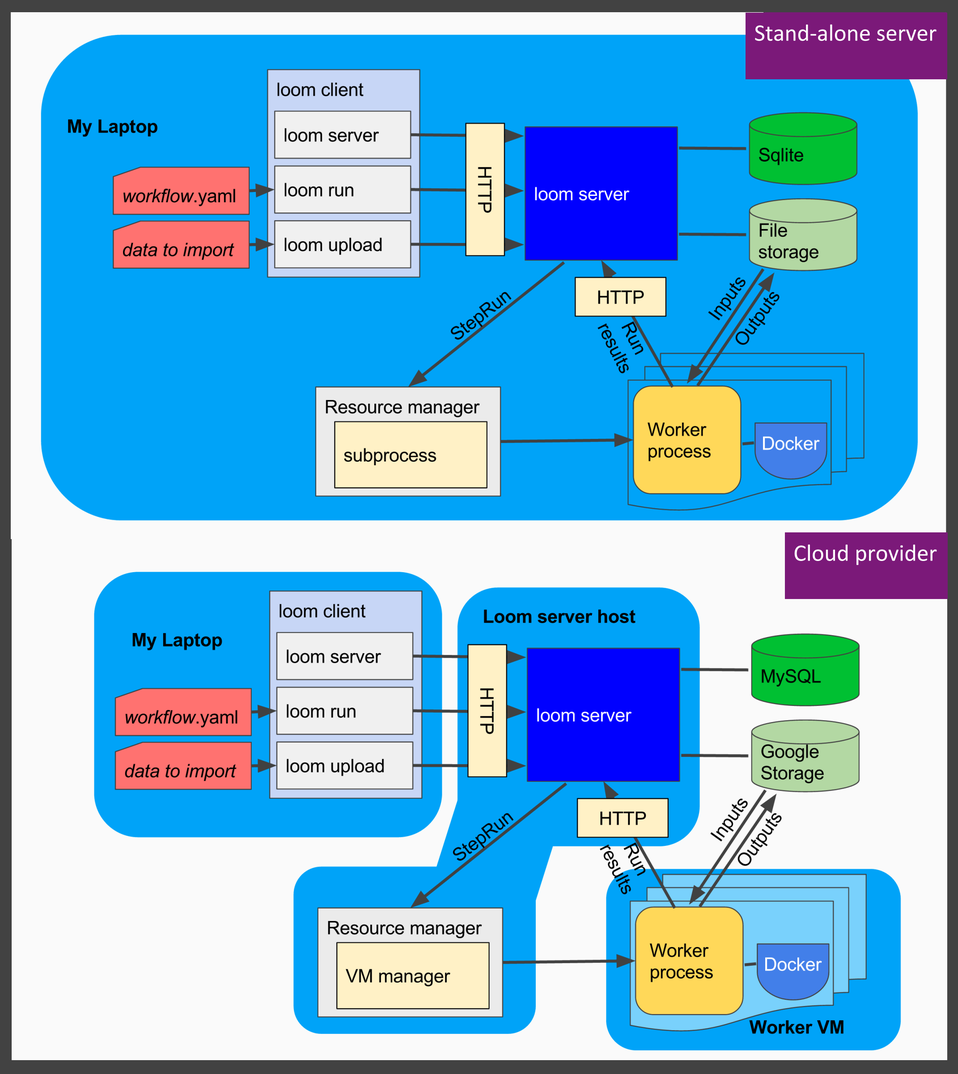



## Portability architecture

With Loom, the same workflow you run on your laptop can be run in the cloud without modification.




- Loom abstracts platform-level services such as file storage, compute, and database operations. With simple adaptors, it can run on many different platforms.
- Loom's client-server architecture allows it to scale from a single user running it on one desktop to many users sharing a remote Loom server.




## Reproducibility & Traceability

To reproduce an analysis, you need to reassemble and verify:

- Input data
- Runtime environment
- Commands executed

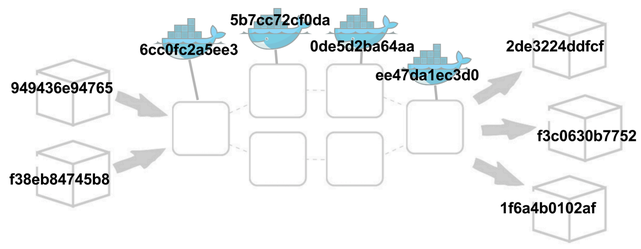
Loom automatically keeps track of these for you.

Files are always identified by hash, and verified by default.

Runtime environment is saved using Docker and tracked by an immutable image ID.

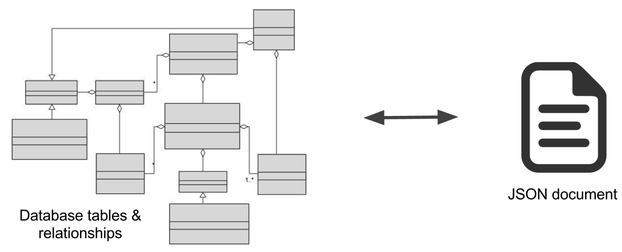
### Content-addressed external resources

Objects too large to be saved in the database are always tracked by a unique hash of their contents

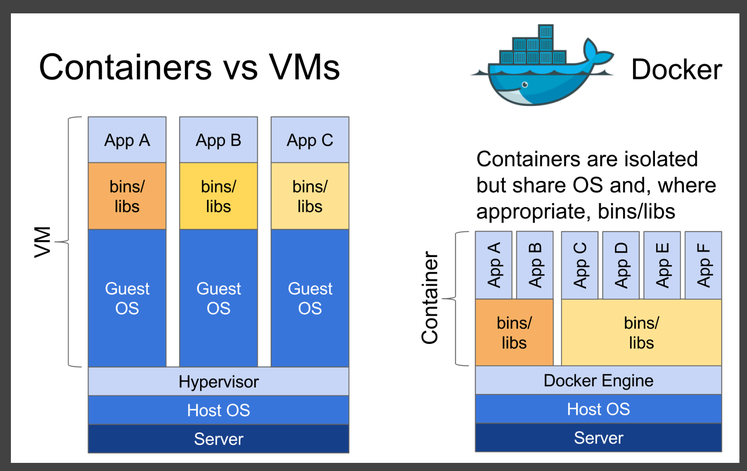



### Built-in serialization/deserialization of database records

Allows logging all database info without loss of information, allows logged records to be restored



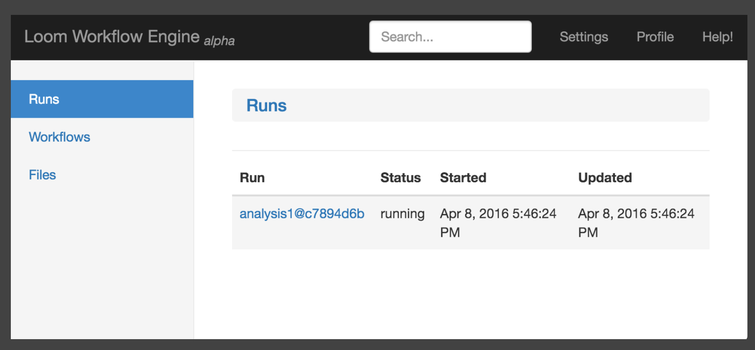

Docker makes runtime environments both portable and reproducible.




## Getting started

Loom is still in pre-release but we invite you to check it out and let us know what you think!

You can find us on github:
https://github.com/StanfordBioinformatics/loom




## Resources

Stanford Center for Genomics and Personalized Medicine
http://scgpm.stanford.edu/

https://github.com/StanfordBioinformatics/loom
https://pypi.python.org/pypi/loomengine

## Special thanks to our partners

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